

Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chp6>
RPI-83M4 is from the library RPI-1 constructed by the group of
Pleier de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>

VECTOR: pCYPAC2
IMPORTANT: This sequence is not the entire insert of clone RPI-83M4
It may be shorter because we sequence overlapping sections only
once, except for a 100 base overlap.
The true left end of clone RPI-83M4 is at 1 in this sequence. The
true left end of clone RPI-91J74 is at 104129 in this sequence.

FEATURES

```
Source      Location/Qualifiers
1..104228
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/clone="RPI-83M4"
/clone_lib="RPI-1"
repeat_region 1302..1605
    /note="AluX repeat: matches 1..303 of consensus"
repeat_region 2223..2533
    /note="L2 repeat: matches 1866..2190 of consensus"
repeat_region 2573..2617
    /note="MIR repeat: matches 202..247 of consensus"
repeat_region 2581..2634
    /note="L2 repeat: matches 2693..2747 of consensus"
repeat_region 2637..2861
    /note="MIR repeat: matches 1..262 of consensus"
repeat_region 3966..4024
    /note="AluY/FLAM repeat: matches 35..77 of consensus"
repeat_region 4613..4720
    /note="L2 repeat: matches 1..278 of consensus"
repeat_region 4759..5035
    /note="AluX repeat: matches 1..278 of consensus"
repeat_region 5613..5697
    /note="MIR repeat: matches 65..150 of consensus"
repeat_region 5746..6018
    /note="L2 repeat: matches 169..450 of consensus"
repeat_region 6681..6805
    /note="MIR repeat: matches 61..185 of consensus"
repeat_region 7197..7476
    /note="L2 repeat: matches 2355..2530 of consensus"
repeat_region 7544..7704
    /note="L2 repeat: matches 2609..2746 of consensus"
repeat_region 8707..8977
    /note="AluX repeat: matches 1..268 of consensus"
repeat_region 10041..10339
    /note="AluX repeat: matches 1..301 of consensus"
repeat_region 11963..12086
    /note="FLAM repeat: matches 1..124 of consensus"
repeat_region 12102..12143
    /note="AluX repeat: matches 98..142 of consensus"
repeat_region 12144..12456
    /note="AluX repeat: matches 1..304 of consensus"
repeat_region 12457..12617
    /note="AluX repeat: matches 142..282 of consensus"
repeat_region 12648..12786
    /note="L2 repeat: matches 2596..2745 of consensus"
repeat_region 13356..13668
    /note="AluX repeat: matches 1..310 of consensus"
repeat_region 13845..14157
    /note="AluX repeat: matches 1..313 of consensus"
repeat_region 14484..14623
    /note="MIR repeat: matches 70..212 of consensus"
repeat_region 15188..15497
    /note="AluX repeat: matches 1..311 of consensus"
repeat_region 15498..15557
    /note="L2 repeat: matches 2007..2143 of consensus"
repeat_region 15931..16276
    /note="L2 repeat: matches 6099..6167 of consensus"
repeat_region 15931..16276
    /note="MIR repeat: matches 2383..2731 of consensus"

repeat_region 16277..16587
    /note="AluX repeat: matches 6..312 of consensus"
repeat_region 16588..18382
    /note="MIR repeat: matches 627..2383 of consensus"
misc_feature 16997..17123
    /note="Sequence from overlapping clone B3B1 (AL512354).  
Assembly confirmed by restriction digest."
repeat_region 18383..18643
    /note="MIR repeat: matches 7..275 of consensus"
repeat_region 18644..19263
    /note="MIR repeat: matches 1..627 of consensus"
repeat_region 19527..19632
    /note="MIR repeat: matches 154..258 of consensus"
repeat_region 20848..20937
    /note="MIR repeat: matches 146..240 of consensus"
repeat_region 20940..21242
    /note="MIR repeat: matches 70..429 of consensus"
repeat_region 22808..23017
    /note="MIR repeat: matches 70..284 of consensus"
repeat_region 23035..23336
    /note="MIR repeat: matches 1..309 of consensus"
repeat_region 23523..23658
    /note="MIR repeat: matches 1..139 of consensus"
repeat_region 23659..23917
    /note="MIR repeat: matches 21..285 of consensus"
repeat_region 24084..24278
    /note="MIR repeat: matches 1..195 of consensus"
repeat_region 25005..25087
    /note="MIR repeat: matches 92..185 of consensus"
repeat_region 26139..26440
    /note="MIR repeat: matches 1..299 of consensus"
repeat_region 26889..27041
    /note="MIR repeat: matches 78..252 of consensus"
repeat_region 27623..28017
    /note="MIR repeat: matches 1..364 of consensus"
repeat_region 29032..29383
    /note="MIR repeat: matches 1..354 of consensus"
repeat_region 29985..30289
    /note="MIR repeat: matches 1..307 of consensus"
repeat_region 30313..30457
    /note="MIR repeat: matches 2..189 of consensus"
repeat_region 32411..33100
    /note="MIR repeat: matches 5426..6134 of consensus"
repeat_region 33301..33442
    /note="MIR repeat: matches 71..232 of consensus"
repeat_region 34707..34752
    /note="MIR repeat: matches 23 copies 2 mer tt 76% conserved"
repeat_region 34819..34990
    /note="MIR repeat: matches 5972..6143 of consensus"
repeat_region 34992..35031
    /note="MIR repeat: matches 10 copies 4 mer aaat 85% conserved"
repeat_region 35362..36232
    /note="MIR repeat: matches 1..426 of consensus"
repeat_region 37387..37697
    /note="MIR repeat: matches 1..311 of consensus"
repeat_region 37710..37993
    /note="MIR repeat: matches 1..286 of consensus"
repeat_region 38849..39089
    /note="MIR repeat: matches 2..262 of consensus"
repeat_region 40658..40945
    /note="MIR repeat: matches 1..288 of consensus"
repeat_region 41221..41256
    /note="MIR repeat: matches 1806..1889 of consensus"
repeat_region 41267..41347
    /note="MIR repeat: matches 1806..1889 of consensus"
repeat_region 41323..41464
    /note="MIR repeat: matches 2007..2143 of consensus"
repeat_region 41487..41557
    /note="MIR repeat: matches 6099..6167 of consensus"
repeat_region 41558..41965
    /note="MIR repeat: matches 1..426 of consensus"
```

/db_xref="GI:3248918"
 /translation="MKDRLAELLDLSKQYDQFPDGDDEPDSPHEDIYETDHIIESL
 YRIDIDENOLIVADVRLKQNAFLTSMRLSSIKRDNLSAKARAGEVTHC
 KLRAMELSEAAOHPHSAVARISRAQYNALTLTFORAMHDYNOAEMKRONCKIR
 IOROLEIMKEVSGDOIEMFEGQKMDVSENLADYKRGCPPTSRRAATNCCAMR
 AAIKRVHELFIDMAVLEKQADTLNVIETLNQKTYDITGQAKQVRYEKNPCR
 TLCCFCCPCLK"
 BASE COUNT 281 a 409 c 399 g 191 t
 ORIGIN

Query Match 44.1%; Score 570.6; DB 9; Length 1280;
 Best Local Similarity 98.9%; Pred. No. 1.6e-79;
 Matches 606; Conservative 0; Mismatches 4; Indels 3; Gaps 3;

OY 1 acccagcgccagctgagatcatggaaggaagtcctcgccgagccagatcgaggaatg 60
 Db 664 ATCCAGCCGACGTGAGATCATGAGGCAAGAGTCTCGGCGCACGATCGAGGACATG 723
 OY 61 ttcgagcagggaagtgagagcgtgtttccgagaacttgctgagcagcgtgaaggcgcg 120
 Db 724 TTCCGAGCAGGTAAGTGGACGCTTTCCGAGAACTTGCTGGCCGCGAGGAGGCG -CG 782
 OY 121 cggcgccgctcaagagatcgagagccgcccagcgaactgtgagcctgagagagcg - 179
 Db 783 CGGCGCGCCACACGAGATCGAGAGCCCGCACCGCAACTGCTGCGCTGAGAGCGCG 842
 OY 180 catccgagcagctacagagatctctctgagatgagcgtgagtgaggaagcagcgca 239
 Db 843 CATCCGCGAGATACAGACACTCTCTTTCAGATGCGGCTGCTGAGAGAGAGCGCGA 902
 OY 240 caacctgaagcgtcatgagctcaagtcacaaagacggtgactacacggcgagcgcaa 299
 Db 903 CACCTGAAAGCTATGAGCTCAACCTACAAAAGACGGTGTGACTACCGCGGCGGCGCAA 962
 OY 300 ggcgagagtgaggaagcggctgacagagagaggaagaccctgagcggagcctctgctg 359
 Db 963 GCGCAGAGTGGAGAGGCGGTGACGAGAGAGAACCCCTGCGGAGCCTCTGCTG 1022
 OY 360 ctctgctgctccctgctcctcaagtagcagagcgccgagcgccgagcccatccagagc 419
 Db 1023 CTTCGTGCTGCTGCTGCTCAAGTAGAGGCGCGCGCGCGCGCCACGCCCATCCAGAC 1082
 OY 420 catgagagcgtctggaagagcgtcaacaaagccggagagctctgcccctgaggaagtg 479
 Db 1083 CATGAGAGCGCGCTGGAGAGAGCG -CACCAAGCGCGGAGCTGCGCTCGAGGAGAGTTGC 1141
 OY 480 cccaacccttcggaaccagctcttagaagaagaagcggaggtcaagaattgcaaac 539
 Db 1142 CCCAACCCCTTCCGGAATCAGCTCTTTAGAAAAGAAAGCCAGGTTCAAAATTGCAAC 1201
 OY 540 cagcctgctgctggaagaatggttagttgataccgtccgagtgattcttcagtaagaatg 599
 Db 1202 CAGCCTGTCTTGGAAAGATGTTACTTGTATACCCGTCATGTATCTTCTCAAGTAAGTAG 1261
 OY 600 attcccaacaagt 612
 Db 1262 ATTCACACCTCGT 1274

RESULT 4
 AF071504 1000 bp mRNA linear PRI 22-JUN-1998
 LOCUS AF071504
 DEFINITION Homo sapiens syntaxin 11 mRNA, complete cds.
 ACCESSION AF071504
 VERSION AF071504.1 GI:3243239
 KEYWORDS human.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1000)
 AUTHORS Valdez,A.C., Cabanlois,J.-P., Brown,M.J. and Roche,P.A.

TITLE Syntaxin 11 is a novel SNARE protein associated with the
 Trans-Golgi network and late endosomes
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1000)
 AUTHORS Valdez A.C., Cabanlois,J.-P., Brown,M.J. and Roche,P.A.
 TITLE Direct Submission
 JOURNAL Submitted (10-JUN-1998) NCI/EIB, NIH, 10 Center Drive, Bethesda, MD
 20892, USA

FEATURES
 source
 1..1000
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /tissue_type="placenta"
 55..918
 /note="SNARE protein"
 /codon_start=1
 /product="syntaxin 11"
 /protein_id="AAC24004.1"
 /db_xref="GI:3243240"
 /translation="MKDRLAELLDLSKQYDQFPDGDDEPDSPHEDIYETDHIIESL
 YRIDIDENOLIVADVRLKQNAFLTSMRLSSIKRDNLSAKARAGEVTHC
 KLRAMELSEAAOHPHSAVARISRAQYNALTLTFORAMHDYNOAEMKRONCKIR
 IOROLEIMKEVSGDOIEMFEGQKMDVSENLADYKRGCPPTSRRAATNCCAMR
 AAIKRVHELFIDMAVLEKQADTLNVIETLNQKTYDITGQAKQVRYEKNPCR
 TLCCFCCPCLK"

BASE COUNT 224 a 327 c 307 g 142 t
 ORIGIN

Query Match 35.0%; Score 453.4; DB 9; Length 1000;
 Best Local Similarity 99.0%; Pred. No. 2.9e-61;
 Matches 465; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 atccagcgccagctgagatcatggaaggaagtcctcgccgagccagatcgaggaatg 60
 Db 535 ATCCAGCGCCAGCTGAGATCATGAGGCAAGAACTCTCGGCGCACGATCGAGGACATG 594
 OY 61 ttcgagcagggaagtgagagcgtgtttccgagaacttgctgagcagcgtgaaggcgcg 120
 Db 595 TTCCGAGCAGGTAAGTGGAGAGCTTTTCCGAGAACTTGCTGCGCGAGTGAAGGCGCG 654
 OY 121 cggcgccgctcaagagatcgagagccgagcggagcgaactgtgagcctggaagagcg 180
 Db 121 GCGCAGAGTGGAGAGGCGGTGACGAGTGTTCGAGAACTTGCTGCGCGAGTGAAGGCGCG 654
 OY 181 atccgagcagctacagagcctctcttcagatgagcgtgtgctgtggaaggaagcgagc 240
 Db 655 GCGGCGCCCTCAACGAGATCGAGAGCGCCACCGCAACTGCTGCGCTGAGAGCGCG 714
 OY 715 ATCCGCGACGTACAGAGCTCTTCTTCAAGATGGCGGTGCTGTGGAGAGAGCGGAC 774
 OY 241 accctgaagctcatcgagctcaacgtaacaaagcgttcgactacacggcgagcgcaag 300
 Db 775 ACCCTGAACGTCAATCGAGCTCAACGTACAAAAGAGCGGTGAGCTACACGGCGAGCGCAAG 834
 OY 301 ggcgagtgctggaagcgcgtgagtaagagagaagaaacccctgagcagccctctgctgc 360
 Db 835 GCGCAGGTGGAGAGGCGGTGAGTACGAGAGAGAAACCCCTGCGAGACCTTCTGCTGC 894
 OY 361 ttcgctgctccctgctcctcaagtagcagcgccgagcgccgagcggccatcccaaac 420
 Db 895 TTCTGCTGCTGCTGCTCAAGTACAGGCGCGGCGCGCGCGCACCCCATCCCAAC 954
 OY 421 atgagcgcgctggaagagcgtcaacaaagcggagcgtgagcct 467
 Db 955 ATGAGCGCGCTTGGAGAGAGCG -CACCAAGCGCGGAGAGCTGTGCGCT 1000

RESULT 5
 AC091681 207379 bp DNA linear HMG 29-JAN-2002
 LOCUS AC091681
 DEFINITION Mus musculus chromosome 10 clone rp23-111d4 strain C57BL/6J,
 WORKING DRAFT SEQUENCE, 29 unordered pieces.
 ACCESSION AC091681
 VERSION AC091681.27 GI:18390231

QY 657 cagaagccaaagtaaggaactgaagtgatctgactgtgagggtgaaatgcttgagccgtgc 716
DB 92016 AGCAACTAAGGTCATTGGT--AAGATGTGTCTTTGAAGAGGAGCAACCAAGAACAGG 92074
QY 717 ctccctata----aagactaaaggaggaactgaatggcactgcctaatagaaatgact 772
DB 92075 ATGCTTAATAGTATGAGACATTTTCANAAAGTTGCTTTGTTATCCCTCTGGAAAGTTC 92134
QY 773 catgatggaacttcagttcaattacttctccctgaaactccctgtctgtccatc 832
DB 92135 CTTGGTGCTATATGTTTGAATGACATT--CACTTCAGTAATTAATTCAGTCTGTTCAATT 92193
QY 833 ttgagcgaatctggccttgggaaaccac-gttctcctccctccgattctcagcgtc 891
DB 92194 TCGTGAACCTTTGCTGGGTAATTTGGCTGCATTCACCTTCGATTAATTAATTTGTTGTC 92253
QY 892 taagtgatgcaatctcctcccaataagatctattctgtcgcattcccccactat 951
DB 92254 TGAAG-----CCCTGCGTGAACCTCCTCCCTTGCGCTCCGCTCCACATACACAG 92299
QY 952 taaatcacacacaaactactactatcttctatctcttcaacttttaaatcttcac 1011
DB 92300 TA-----ACCCCTACATGAGACATGGCTCCTTACCTCTCACCCTTT--ATATGTCAC 92352
QY 1012 caggtatattctgattatttcccaaacattttaagcaactgaatcgcgaagca 1071
DB 92353 CAGCTTAATATGAAATAT-----TTTAAACACCAATATTTGAACAAGCA 92398
QY 1072 ctcaaatlta---agtaacgaatcgtttgtgatttttgcgtgataaaattatta 1127
DB 92399 CTCMACTTGACCTTTATATGGTCACATTTTATGAGATTTTTCACAGTAACATTATTTA 92458
QY 1128 acattataatttactgattacatgacatgtaataatgtaataactaact 1187
DB 92459 AATTTATCTTTGTTACTTATTCATATGATGATATGGTGAATGTAA---ACTAATCTC 92515
QY 1188 caactaatatgtaca-taagtacaaatggttaactctcttaagtatgtatata 1246
DB 92516 CATTCCTATGCTTACATTAATGCGCAATTAATGATTAAGTCTTTTGAAATCTGTATA 92575
QY 1247 taattccaaga 1258
DB 92576 TAAACACAAAGA 92587

RESULT 6
LOCUS AF038898 864 bp mRNA linear PRI 05-JAN-1999
DEFINITION Homo sapiens syntaxin 11 mRNA, complete cds.
ACCESSION AF038898
VERSION AF038898.1 GI:4104684
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Tang,B.L., Low,D.Y., Lee,S.S., Tan,A.E. and Hong,W.
TITLE Direct Submission
JOURNAL Submitted (16-DEC-1997) Institute of Molecular and Cell Biology, 30
Medical Drive, Singapore 117609, Republic of Singapore
FEATURES
source
1..864
/organism="Homo sapiens"
/db_xref="taxon:9606"
1..864
/codon_start=1
/product="syntaxin 11"
/protein_id="AAD02107.1"
/db_xref="GI:4104685"
/translation="MKDRAELLDLSKOYDOOPGDDDFSDPHEDIVETDHIESTL
YRDIIDIDENOLLVANKRKLKONRKLFLTSMRLSTIRDTNLSINKAKAPEVTHC
NVRAMELSEAEAOHGPALSGGISRAQYNALTLTFORAMHDYNOAEMKORNDCKIR

IOHOLEIMGEVSDQIEDMEFQKMDVFSNNLADYKGVRAALNETESRRRLVRL
SAIRDVHELELOMAVLEVKQADTLNVLELNVQKTVDTGAKAORAVOYEERNPGR
TLCEFCPCPK"

BASE COUNT 201 a 272 c 262 g 129 t

ORIGIN

Query Match 28.9%; Score 374.4; DB 9; Length 864;
Best Local Similarity 98.4%; Pred. No. 5.7e-49;
Matches 378; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 atccagcgccagcttggagatcatgaggaagaatctcggcgaccagatcggagacatg 60
DB 481 ATCCAGCGCCAGCTGGAGATCATGGCAAGAGTCTGGGCGACACATCGACGACATG 540
QY 61 ttgagcagggtaatgtagctgtttctcagaaacttgcctggcgagctgaaggcg 120
DB 541 TTCAGCAGGGTAAAGTGAGGAGCTGTTTCCGAAACTTGCTGGCCGAGTGAAAGGTTG 600
QY 121 cggcgccctcaacagagatcgaagccgacccgagactgtcgcctggagagccgc 180
DB 601 CGGCGCCGCTCAACAGAGATCGAGAGCCGCCGAACCTGTCGGCTGGAGAGCGCC 660
QY 181 atccgcagctacacagagcttcttcagatgctgtcgtgtgtgagaaagcagc 240
DB 661 ATCCGCGAGTACAGAGACTCTTCTGCAGATGGCGGTGCTGTGAGAAAGCAGCGCAG 720
QY 241 accctgaacgcatcagactcaacgtacaaaagcgtcagactacacggcgcaaggc 300
DB 721 ACCCTGAACGTCATCGACTCACTACAAAAGAGGTGCACTACCGCGCCAGGCCAAG 780
QY 301 gcgcaggtcgcgaagcgcttgcagtaacgaagaacccctgcgcgaccctcgtcgc 360
DB 781 GCGCAGGTCGGAAGCGCGTCAGACGAGAGAAAGAACCCCTGCCGAGACCTCTGCTGC 840
QY 361 ttctgctgtccctgcctcaagtag 384
DB 841 TTCTGCTGTCCCTGCCCTCAAGTAG 864

RESULT 7
LOCUS HSA012501 240 bp mRNA linear PRI 09-JUL-1999
DEFINITION Homo sapiens mRNA activated in tumor suppression, clone TSAp21.
ACCESSION AJ012501
VERSION AJ012501.1 GI:5441361
KEYWORDS tumor suppression.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Koperch,J.P., Lethone,F., Pigneur,S., Plouffe,L., Israeli,D.,
Tuynder,M., Nemanl,M., Pasturaud,P., Gendron,M.C., Dausset,J.,
Oren,M., Amson,R.B. and Teitelman,A.
TITLE SIAH-1 promotes apoptosis and tumor suppression through a network
involving the regulation of protein folding, unfolding, and
trafficking: identification of common effectors with p53 and
p21(Waf1)
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (14), 8070-8073 (1999)
MEDLINE 99324190
REFERENCE 2 (bases 1 to 240)
AUTHORS Amson,R.B.
TITLE Direct Submission
JOURNAL Submitted (22-OCT-1998) Amson R.B., Tumor Suppression, CEPH Human
Polymorphism Study Center, 27 rue Juliette Doda Paris, 75010, FRANCE
FEATURES
source
1..240
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="K562"
/clone="TSAp21"
39..44
polya_signal

|||||
Db 448 ATCCAGCGCAGCTAGAGATCACTGGAGAGACCACCACTGACGAGGAGCTGGAGGAGATG 507
QY 61 ttcgagcaggtgaagtggagcgtgtttccgagaacttgctggccagcgtgaagggcgcg 120
Db 508 CTGGAGAGCGGGAGAGCGCCATCTTCATCTCGGACATATATACATATTACAGATTACT 567
QY 121 cggagcggccctcaacagagatcgagagcgccacccggaactgctgcccctggagagcgcg 180
Db 568 AGGCAAGCTCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 627
QY 181 atccgagcagctacagagctcttcttcgagagatggcggtgctggtggagagagcgcgac 240
Db 628 ATCCGAGAGCTCAGCAGATGTTATGATGATGATGATGATGATGATGATGATGATGATG 687
QY 241 acccgaagcgtacagcagctacacaaagagcagcagcagcagcagcagcagcagcagcag 300
Db 688 ATGCTCAACACATTCAGAGAAACGTGGTAACCTCGTGAATTACCTGGAGCAGCCCAAG 747
QY 301 gcgcaggtggcgaagcgctgagctacgagagagagagagagagagagagagagagagag 360
Db 748 GAAGAGACTAAGAAAGCCATCAATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 807
QY 361 ttcgtcttcctgc 375
Db 808 CTCGGCCAGCAGCTGC 822

RESULT 10
AR111444
LOCUS AR111444 486 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 13 from patent US 6127149.
ACCESSION AR111444
VERSION AR111444.1 GI:12828292
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 486)
AUTHORS Hirai, Y., Koshida, S. and Oka, Y.
TITLE Modified epimorphin
JOURNAL Patent: US 6127149-A 13-03-OCT-2000;
FEATURES
Source location/Qualifiers
1..486
BASE COUNT 152 a 110 c 139 g 85 t
ORIGIN

Query Match 9.6%; Score 124.8; DB 6; Length 486;
Best Local Similarity 60.7%; Pred. No. 3.9e-10;
Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;
QY 1 atccagcagcagctgagatcatgagcgaagagctcggcgagcagcagcagcagcagcagcag 60
Db 133 ATCCAGCGCAGCTAGAGATCACTGGAGAGACCACCACTGACGAGCAGCTGGAGAGATG 192
QY 61 ttcgagcaggtgaagtggagcgtgtttccgagaacttgctggccagcgtgaagggcgcg 120
Db 193 CTGGAGAGCGGGAGAGCGCCATCTTCATCTCGGACATATATACATATTACAGATTACAA 252
QY 121 cggagcggccctcaacagagatcgagagcgccacccggaactgctgcccctggagagcgcg 180
Db 253 AGGCAAGCTCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 312
QY 181 atccgagcagctacagagctcttcttcgagagatggcggtgctggtggagagagcgcgac 240
Db 313 ATCCGAGAGCTCAGCAGATGTTATGATGATGATGATGATGATGATGATGATGATGATG 372
QY 241 acccgaagcgtacagcagctacacaaagagcagcagcagcagcagcagcagcagcagcag 300
Db 373 ATGCTCAACACATTCAGAGAAACGTGGTAACCTCGTGAATTACCTGGAGCAGCCCAAG 432

QY 301 gcgcaggtggcgaagcgctgagctacgagagagagagagagagagagagagagagagag 336
Db 433 GAAG 468
RESULT 11
E12728
LOCUS E12728 486 bp DNA linear PAT 24-JUN-1998
DEFINITION DNA encoding mouse Epimorphin-derived peptide.
ACCESSION E12728
VERSION E12728.1 GI:3251560
KEYWORDS JP 1997065885-A/7.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 486)
AUTHORS Koshida, S., Oka, Y. and Hirai, Y.
TITLE TAILORED DERIVATIVE OF EPIMORPHIN
JOURNAL Patent: JP 1997065885-A 7 11-MAR-1997;
SUMITOMO ELECTRIC IND LTD
COMMENT
OS None
OC Artificial sequences.
PN JP 1997065885-A/7
PD 11-MAR-1997
PF 29-MAR-1996 JP 1996099684
PR 31-MAR-1995 JP 95P 99960, 19-JUN-1995 JP 95P 175540 PI
PC KOSHIDA SHOJO, OKA YUMIKO, HIRAI YOHEI
PC C12N15/09, C07H21/04, C07K7/06, C07K7/08, C07K14/485, PC
C12P21/02//A61K38/00.
PC (C12P21/02, C12R1:19);
CC strandedness: Double;
CC topology: linear;
FH Key location/Qualifiers
FT source 1..486
FT mat_peptide 1..483
FT (23) /product='Epimorphin fragment designated FT
FT /note='fragment (23) is derived from 104-264
FT aa of mouse
FT Epimorphin'.
FEATURES
Source location/Qualifiers
1..486
BASE COUNT 152 a 110 c 139 g 85 t
ORIGIN

Query Match 9.6%; Score 124.8; DB 6; Length 486;
Best Local Similarity 60.7%; Pred. No. 3.9e-10;
Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;
QY 1 atccagcagcagctgagatcatgagcgaagagctcggcgagcagcagcagcagcagcagcag 60
Db 133 ATCCAGCGCAGCTAGAGATCACTGGAGAGACCACCACTGACGAGCAGCTGGAGAGATG 192
QY 61 ttcgagcaggtgaagtggagcgtgtttccgagaacttgctggccagcgtgaagggcgcg 120
Db 193 CTGGAGAGCGGGAGAGCGCCATCTTCATCTCGGACATATATACATATTACAGATTACAA 252
QY 121 cggagcggccctcaacagagatcgagagcgccacccggaactgctgcccctggagagcgcg 180
Db 253 AGGCAAGCTCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 312
QY 181 atccgagcagctacagagctcttcttcgagagatggcggtgctggtggagagagcgcgac 240
Db 313 ATCCGAGAGCTCAGCAGATGTTATGATGATGATGATGATGATGATGATGATGATGATG 372
QY 241 acccgaagcgtacagcagctacacaaagagcagcagcagcagcagcagcagcagcagcag 300
Db 373 ATGCTCAACACATTCAGAGAAACGTGGTAACCTCGTGAATTACCTGGAGCAGCCCAAG 432

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 24, 2002, 14:13:36 ; Search time 237.5 Seconds

(without alignments)
9361.702 Million cell updates/sec

Title: us-09-762-249-13

Perfect score: 1295
Sequence: 1 atccagcgccagctgagat.....aaaaaaaaaaaaaaaaaaaa 1295

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_032802:*

- 1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
- 2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
- 3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
- 4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
- 5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
- 6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
- 7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
- 8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
- 9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
- 10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
- 11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
- 12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
- 13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
- 14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
- 15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
- 16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
- 17: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
- 18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
- 19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
- 20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
- 21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	209.2	16.2	240	AAZ61486	CDNA sequence of t
2	124.8	9.6	486	AAT16088	Mouse epimorphin f
3	124.8	9.6	486	AAT62413	Mouse epimorphin f
4	124.8	9.6	564	AAT16087	Mouse epimorphin f
5	124.8	9.6	564	AAT62412	Mouse epimorphin f
6	124.8	9.6	711	AAT16086	Mouse epimorphin f
7	124.8	9.6	711	AAT62411	Mouse epimorphin f
8	124.8	9.6	798	AAT16090	Mouse epimorphin f
9	124.8	9.6	798	AAT62414	Mouse epimorphin c

10	124.8	9.6	840	AAQ41594	Mouse epimorphin 1
11	124.8	9.6	840	AAQ75249	Mouse epimorphine
12	124.8	9.6	867	AAQ41593	Mouse epimorphin 1
13	124.8	9.6	867	AAQ75248	Mouse epimorphine
14	124.8	9.6	870	AAQ41592	Mouse epimorphin c
15	124.8	9.6	870	AAQ75247	Wild type mouse ep
16	124.8	9.6	2940	AAQ41595	Mouse epimorphin g
17	124.8	9.6	2940	AAQ75250	DNA fragment conta
18	121.6	9.4	911	AAQ41548	Rat syntaxin 2 gen
19	118.4	9.1	2088	AAQ00371	CDNA encoding SNAR
20	117.2	9.1	2097	AAQ01546	Rat syntaxin 1A ge
21	107.2	8.3	1200	AAQ54355	Rat post-synaptic
22	107.2	8.3	3000	AAQ01547	Rat syntaxin 1B ge
23	96.6	7.5	486	AAA89595	Mouse syntaxin 1B ge
24	96.6	7.5	486	AAA89596	Mouse syntaxin 1B ge
25	96.6	7.5	897	AAQ199515	Mouse syntaxin 1B ge
26	96.6	7.5	1219	AAA89551	Mouse syntaxin 1B ge
27	94.4	7.3	486	AAQ16085	Human syntaxin 1B ge
28	94.4	7.3	486	AAQ62409	Human epimorphin f
29	94.4	7.3	564	AAQ16084	Human epimorphin f
30	94.4	7.3	564	AAQ62408	Human epimorphin f
31	94.4	7.3	711	AAQ16083	Human epimorphin f
32	94.4	7.3	711	AAQ62407	Human epimorphin f
33	94.4	7.3	795	AAQ16089	Human epimorphin f
34	94.4	7.3	795	AAQ62410	Human epimorphin f
35	94.4	7.3	834	AAQ75246	Human epimorphin c
36	94.4	7.3	864	AAQ41590	Human epimorphine
37	94.4	7.3	864	AAQ75245	Human epimorphine
38	94.4	7.3	867	AAQ41589	Human epimorphine
39	94.4	7.3	867	AAQ75244	Wild type human ep
40	92.8	7.2	834	AAQ41581	Human epimorphin 1
41	90.6	7.0	892	ABA03884	Human POLY15 nucle
42	90.6	7.0	892	ABA03885	Human POLY16 nucle
43	90.6	7.0	893	ABA03883	Human POLY14 nucle
44	90.6	7.0	1233	AAQ31185	Human diagnostic a
45	89.6	6.9	1054	AAQ01549	Rat syntaxin 3 gen

ALIGNMENTS

RESULT	1
ID	AAZ61486 standard; CDNA; 240 BP.
XX	XX
AC	AAZ61486;
XX	XX
DT	19-JUN-2000 (first entry)
XX	XX
DE	CDNA sequence of tumour suppressor activated pathway gene TSAP21.
XX	XX
XX	Tumour suppressor activated pathway gene; TSAP; apoptosis;
KW	tumour suppression; tumour suppressor inhibited pathway gene; TSIP3;
KW	cancer; antiviral; ss.
XX	XX
OS	Homo sapiens.
XX	XX
PN	FR2782085-A1.
XX	XX
PD	11-FEB-2000.
XX	XX
PF	05-AUG-1998; 98FR-0010077.
XX	XX
PR	05-AUG-1998; 98FR-0010077.
XX	XX
PA	(DAUS-) FOND DAUSSET-CEPH JEAN.
XX	XX
PI	Amson R, Telerman A;
XX	XX
DR	WPI: 2000-208788/19.
XX	XX
PT	Nucleic acid sequences useful for gene therapy of cancer and viral
XX	infections correspond to genes whose expression is induced or inhibited

Query Match 9.6%; Score 124.8; DB 17; Length 711;
Best Local Similarity 60.7%; Pred. No. 4.2e-13;
Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 1 atccagcgccagctggagatcatcgtgcaagaagctctcgccgagccacgacatcgagacatg 60
|||||
DB 358 atccagcgccagctggagatcatcgtgcaagaagctctcgccgagccacgacatcgagacatg 417
|||||
QY 61 ttccagcaggtaagtggagacgtgtttccgagaactgtctggccgacgtgaaagggcg 120
|||||
DB 418 ctggagagcgggagccgcatctcatctcatctgatatattatcagattcacaatact 477
|||||
QY 121 cgggcccctcaacagatcgagagccgacccgacactgtctgcccctggagagccgc 180
|||||
DB 478 aggaagctctcaatgagatcgagtcgccgacaaagacatcagagctggagaccagc 537
|||||
QY 181 atccgagcgtacagcagctcttcttcgagatggcggtgtgtgtgagagagcagccagc 240
|||||
DB 538 atccgagagctgacagagatggtcagatagatagcagatgttctgagacatcaggtgaa 597
|||||
QY 241 accctgaagctacagcagctccttcgagatgagcagacggtcgtacacggccagccag 300
|||||
DB 598 atggtcaacaacatcgagagaatgtgtgtaactctgtagattacgtggaaatcgccaag 657
|||||
QY 301 gcgcaggtgcggaagcgctgcaagtacagagagaag 336
|||||
DB 658 gaagagacgaagaagccatcaataacagagcaag 693
|||||

RESULT 7
AAT62411
ID AAT62411 standard; cDNA; 711 BP.
XX
AC AAT62411;
XX
DT 02-JUL-1997 (first entry)
XX
DE Mouse epimorphin truncated variant 2M coding sequence.
XX
KW Human; mouse; epimorphin; coiled-coil region; functional domain; tissue;
KW hydrophobic; deletion; truncation; regulation; morphogenesis; epithelium;
KW artificial organ; cosmetic; hair tonic; ds.
OS Synthetic.
XX
PN JP09065885-A.
XX
PD 11-MAR-1997.
XX
PR 29-MAR-1996; 96JP-0099684.
XX
PR 19-JUN-1995; 95JP-0175540.
XX
PR 31-MAR-1995; 95JP-0099980.
XX
PA (SUME) SUMITOMO ELECTRIC IND CO.
XX
DR WPI; 1997-220419/20.
XX
DR P-PSDB; 14260.
XX
PT Modified epimorphin and related DNA - useful e.g. for treatment of
XX tissues or in artificial organs, or as an ingredient in cosmetics
XX
PS Example 1; Page 13; 18pp; Japanese.

The invention relates to novel human (AAW14257-9) or mouse (AAW14260-2) epimorphin proteins with replacements, deletions or substitutions in the amino acid sequence. The new epimorphin protein consists of: (a) an N-terminal coiled-coil region; (b) a functional domain in the middle; and (c) a C-terminal coiled-coil region. A hydrophobic region in the C-terminal has been deleted and at least some amino acids have been deleted from the terminals of coiled coil regions (a) and/or (c). This sequence encodes the mouse epimorphin protein lacking the N-terminal 29 amino acids. Epimorphin is a protein which regulates morphogenesis

CC of epithelial tissues. It can be used for treatment of tissues or used
CC directly in artificial organs or as an ingredient in cosmetics, hair
CC tonic, etc.
XX
SQ Sequence 711 BP; 232 A; 155 C; 201 G; 123 T; 0 other;

Query Match 9.6%; Score 124.8; DB 18; Length 711;
Best Local Similarity 60.7%; Pred. No. 4.2e-13;
Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 1 atccagcgccagctggagatcatcgtgcaagaagctctcgccgagccacgacatcgagacatg 60
|||||
DB 358 atccagcgccagctggagatcatcgtgcaagaagctctcgccgagccacgacatcgagacatg 417
|||||
QY 61 ttccagcaggtaagtggagacgtgtttccgagaactgtctggccgacgtgaaagggcg 120
|||||
DB 418 ctggagagcgggagccgcatctcatctcatctgatatattatcagattcacaatact 477
|||||
QY 121 cgggcccctcaacagatcgagagccgacccgacactgtctgcccctggagagccgc 180
|||||
DB 478 aggaagctctcaatgagatcgagtcgccgacaaagacatcagagctggagaccagc 537
|||||
QY 181 atccgagcgtacagcagctcttcttcgagatggcggtgtgtgtgagagagcagccagc 240
|||||
DB 538 atccgagagctgacagagatggtcagatagatagcagatgttctgagacatcaggtgaa 597
|||||
QY 241 accctgaagctacagcagctccttcgagatgagcagacggtcgtacacggccagccag 300
|||||
DB 598 atggtcaacaacatcgagagaatgtgtgtaactctgtagattacgtggaaatcgccaag 657
|||||
QY 301 gcgcaggtgcggaagcgctgcaagtacagagagaag 336
|||||
DB 658 gaagagacgaagaagccatcaataacagagcaag 693
|||||

RESULT 8
AAT16090
ID AAT16090 standard; cDNA; 798 BP.
XX
AC AAT16090;
XX
DT 06-JUN-1996 (first entry)
XX
DE Mouse epimorphin fragment (123).
XX
KW Epimorphin; human; mouse; wound; burn; epithelial tissue;
KW diagnosis; treatment; morphogenetic abnormality; cosmetic;
KW hair growth stimulator; ds.
XX
OS Mus musculus.
XX
PN EP698666-A2.
XX
PD 28-FEB-1996.
XX
PF 20-JUN-1995; 95EP-0304270.
XX
PR 31-MAR-1995; 95JP-0099980.
XX
PR 21-JUN-1994; 94JP-0162874.
XX
PR 31-MAR-1995; 95JP-0099979.
XX
PA (SUME) SUMITOMO ELECTRIC IND CO.
XX
PI Hirai Y, Koshida S, Oka Y;
XX
DR WPI; 1996-118213/13.
XX
PT Novel polypeptide containing an epimorphin functional domain - has
XX possible benefits in epithelial tissue treatments, e.g. burns and
XX for artificial organs
XX
PS Claim 27; Page 51; 62pp; English.

```

XX  W09308213-A.
PN
XX
XX  29-APR-1993.
PD
XX
XX  15-OCT-1992; 92WO-JP01340.
PF
XX  16-OCT-1991; 91JP-0294856.
PR  16-OCT-1991; 91JP-0294857.
PR  17-APR-1992; 92JP-0122906.
PR  30-APR-1992; 92JP-0135692.
XX
XX  (BIOM-) BIOMATERIAL RES INST CO LTD.
PA
XX  Hirai Y, Takashina M, Takebe K;
PI
XX  WPI; 1993-152423/18.
DR
XX  P-PSDB; AAR36554.
XX
PT  Novel active substance epimorphin, its gene and antibodies - for
PT  diagnosing and treating epithelial diseases
XX
XX  Claim 10; Page 57; 76pp; Japanese.
XX
CC  This sequence encodes one of three isolated isoforms of mouse
CC  epimorphin, a protein produced by mesenchymal cells and which
CC  induces epithelial tissue morphogenesis. Modified forms of
CC  epimorphin in which the C-terminal hydrophobic region is replaced
CC  by a defective or non-hydrophobic peptide are also claimed.
CC  See also AAQ41592 and AAQ41593.
XX
SQ  Sequence 840 BP; 258 A; 193 C; 238 G; 151 T; 0 other;

Query Match
Best Local Similarity 9.6%; Score 124.8; DB 14; Length 840;
Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

OY  1 atccagcgccagctgtagatcatggaagaagctcggcgccagccagatcgagacatg 60
DB  445 atccagcgccagctgtagatcatggaagaagctcggcgccagccagatcgagacatg 504
OY  61 ttcgagcaggtgaagtggagacgtgttttcggaactgtgtgcccgtggaaggcg 120
DB  505 cggagagcgaggagccgtccatctcattcgtgatatattatcagattcacaataact 564
OY  121 cggcgccctcaacgagatcgagagcgccgacgcggaactgtgtgcccgtggaaggcg 180
DB  565 aggcgaagctcgaatgagatcgagctcccgccacaagaacatcatgaagctggaaccagc 624
OY  181 atccgagacgtacacgagctcttcttcgagatggtggtgtgtgagaaagcgccgac 240
DB  625 atccgagagctgtagagatgttcatctgcatatggtcattgttcgagactcgggtgaa 684
OY  241 accctgaagctatcgagctcaacgtacaaaagaacgtgcactacacgcgcgagcaag 300
DB  665 atggtcaacaacaatcgaggaatgtgtgaactctgttaattacgttgaacaatgccaag 744
OY  301 ggcaggtgctggaagcgctgcatgtagaggaag 336
DB  745 gaagagcgaagaagaagcacaataaccagagcaag 780

```

RESULT 11

AAQ75249
AAQ75249 standard; cDNA; 840 BP.

AAQ75249;

10-AUG-1995 (first entry)

Mouse epimorphin isoform B gene.

```

KW  Probe; epimorphin; human; mouse; lambda-gt11; expression library;
KW  monoclonal antibody; isoform; drug; congenital; acquired; E.coli;
KW  epidermal abnormality; ds.
XX
XX  Mus musculus.
OS
XX
XX  Key
FH  Location/Qualifiers
FT  variation 790..840
FT  /*tag= a
FT  /note= "sequence variance in isoform B"
XX
XX  JF06293800-A.
PN
XX
XX  21-OCT-1994.
PD
XX
XX  15-OCT-1992; 92JP-0301581.
PF
XX  15-OCT-1992; 92JP-0301581.
PR
XX  15-OCT-1992; 92JP-0301581.
XX
XX  (BIOM-) BIOMATERIAL KENKYUSHO KK.
PA
XX
XX  WPI; 1995-009638/02.
DR  P-PSDB; AAR66481.
DR
XX
XX  Human or murine epimorphin - useful for development of drugs to
XX  treat congenital and acquired epidermal form abnormality
XX
XX  Claim 10; Page 8-9; 41pp; Japanese.
XX
CC  The sequence of the gene encoding mouse epimorphin isoform B. A DNA
CC  fragment (AAQ75250) containing the mouse epimorphin gene (AAQ75247) was
CC  isolated from a lambda-gt11 expression cDNA library screened with a
CC  monoclonal antibody raised against mouse epimorphin. A probe
CC  (AAQ75243) derived from the mouse gene sequence was used to isolate
CC  isoforms of the mouse gene (AAQ75248-9) and the gene encoding human
CC  epimorphin (AAQ75244) and isoforms (AAQ75245-6). The genes were cloned
CC  into expression systems for the production of the protein in E.coli and
CC  in animal cells. The epimorphin can be used in the development of drugs
CC  to treat both congenital and acquired epidermal form abnormality.
XX
SQ  Sequence 840 BP; 258 A; 193 C; 238 G; 151 T; 0 other;

Query Match
Best Local Similarity 9.6%; Score 124.8; DB 16; Length 840;
Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

OY  1 atccagcgccagctgtagatcatggaagaagctcggcgccagccagatcgagacatg 60
DB  445 atccagcgccagctgtagatcatggaagaagctcggcgccagccagatcgagacatg 504
OY  61 ttcgagcaggtgaagtggagacgtgttttcggaactgtgtgcccgtggaaggcg 120
DB  505 cggagagcgaggagccgtccatctcattcgtgatatattatcagattcacaataact 564
OY  121 cggcgccctcaacgagatcgagagcgccgacgcggaactgtgtgcccgtggaaggcg 180
DB  565 aggcgaagctcgaatgagatcgagctcccgccacaagaacatcatgaagctggaaccagc 624
OY  181 atccgagacgtacacgagctcttcttcgagatggtggtgtgtgagaaagcgccgac 240
DB  625 atccgagagctgtagagatgttcatctgcatatggtcattgttcgagactcgggtgaa 684
OY  241 accctgaagctatcgagctcaacgtacaaaagaacgtgcactacacgcgcgagcaag 300
DB  685 atggtcaacaacaatcgaggaatgtgtgaactctgttaattacgttgaacaatgccaag 744
OY  301 ggcaggtgctggaagcgctgcatgtagaggaag 336
DB  745 gaagagcgaagaagaagcacaataaccagagcaag 780

```

RESULT 12

```

Db      565 aggcgaagctctcaatgatgatcgatccgcgcacaagaacatcatgaagctggaagccagc 624
Oy      181 atccgcagctacacagagctctcttcgcagatggcggtgctgtggaagcagagccagc 240
Db      625 atccgcagagctgcagcagatggttcacatgatggaatggttcgttcgagactcaggtgaa 684
Oy      241 accctgaacgtacatcgagctcaacgtacaaagaacggtcgaactacaccgagccagc 300
Db      685 atggtcaacaacatcgaggaatggtgtgaactctgtagattacgtggaacatgccaag 744
Oy      301 ggcgcaggtgcggaagcgctgctgacgtacgaggaag 336
Db      745 gaagagcgaagaagcctacatcaataccagagcaag 780

```

RESULT 14

AAQ41592 standard; cDNA; 870 BP.

AAQ41592;

24-AUG-1993 (first entry)

Mouse epimorphin coding sequence.

vascularisation; induction; epithelial tissue morphogenesis; ds.

Mus musculus.

Location/Qualifiers

1..870

/tag= a

/product= epimorphin

MO9308213-A.

29-APR-1993.

15-OCT-1992;

92WO-JP01340.

16-OCT-1991;

91JP-0294856.

16-OCT-1991;

91JP-0294857.

17-APR-1992;

92JP-0122906.

30-APR-1992;

92JP-0135692.

(BIOM-) BIOMATERIAL RES INST CO LTD.

Hirai Y, Takashina M, Takebe K;

WPI; 1993-152423/18.

P-PSDB; AAR6552.

Novel active substance epimorphin, its gene and antibodies - for

diagnosing and treating epithelial diseases

Claim 10; Page 55; 76pp; Japanese.

This sequence encodes one of three isolated isoforms of mouse

epimorphin, a protein produced by mesenchymal cells and which

induces epithelial tissue morphogenesis. Modified forms of

epimorphin in which the C-terminal hydrophobic region is replaced

by a defective or non-hydrophobic peptide are also claimed.

See also AAQ41593 and AAQ41594.

Sequence 870 BP; 261 A; 192 C; 253 G; 164 T; 0 other;

Query Match 9.6%; Score 124.8; DB 14; Length 870;

Best Local Similarity 60.7%; Pred. No. 4,3e-13;

Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

Oy 1 atccgcagcagctgagatcattggaaggaagctcgcgcagcagcagatcgagacatg 60

```

Db      445 atccgcagcagctgagatcattggaaggaagcaccctcgcgcagcagctggaagagatg 504
Oy      61 ttcgagcaggtgtaatggaagcgtgttccgagacactgctgagcagctgaaagcgcg 120
Db      505 ctggaagcgggaagcgcgtccatctcattcgtgatattatcagattcaacaatact 564
Oy      121 cgggcgcctcaacagatcgagagcgcgcacccgcgaactgctgagcctggaagcgcg 180
Db      565 aggcgaagctctcaatgatgatcgatccgcgcacaagaacatcatgaagctggaagcagc 624
Oy      181 atccgcagctacacagagctcttccagatggtggtgctgtggaagcagcgcgac 240
Db      625 atccgaagctgcagcagatggttcattgatatggttcgttcgagactcaggtgaa 684
Oy      241 accctgaacgtacatcgagctcaacgtacaaagaacggtcgaactacaccgagccagc 300
Db      685 atggtcaacaacatcgaggaatggtgtgaactctgtagattacgtggaacatgccaag 744
Oy      301 ggcgcaggtgcggaagcgcgtgcagtaacgaggaag 336
Db      745 gaagagcgaagaagcctacatcaataccagagcaag 780

```

RESULT 15

AAQ75247 standard; cDNA; 870 BP.

AAQ75247;

10-AUG-1995 (first entry)

Wild type mouse epimorphine gene.

Probe: epimorphine; human; mouse; lambda-gt11; expression library;

monoclonal antibody; isoform; drug; congenital; acquired; E.coli;

epidermal abnormality; ds.

Mus musculus.

JP06293800-A.

21-OCT-1994.

15-OCT-1992;

92JP-0301581.

15-OCT-1992;

92JP-0301581.

(BIOM-) BIOMATERIAL KENKYUSHO KK.

WPI; 1995-009638/02.

P-PSDB; AAR66479.

Human or murine epimorphine - useful for development of drugs to

treat congenital and acquired epidermal form abnormality

Claim 10; Page 8; 41pp; Japanese.

The sequence of the wild type gene encoding mouse epimorphine. A DNA

fragment (AAQ75250) containing the mouse epimorphine gene was isolated

from a lambda-gt11 expression cDNA library screened with a monoclonal

antibody raised against mouse epimorphine. A probe (AAQ75243) derived

from the mouse gene sequence was used to isolate isoforms of the mouse

gene (AAQ75248-9) and the gene encoding human epimorphine (AAQ75244) and

isoforms (AAQ75245-6). The genes were cloned into expression systems for

the production of the protein in E.coli and in animal cells. The

epimorphine can be used in the development of drugs to treat both

congenital and acquired epidermal form abnormality.

Sequence 870 BP; 261 A; 192 C; 253 G; 164 T; 0 other;

Query Match 9.6%; Score 124.8; DB 16; Length 870;

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 24, 2002, 14:12:02 ; Search time 66.07 Seconds

(without alignments)
4814.521 Million cell updates/sec

Title: US-09-762-249-13

Perfect score: 1295

Sequence: 1 atccagcgcagctgagat.....aaaaaaaaaaaaaaaa 1295

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_NA: *
1: /cgn2_6/ptodata/2/lna/5b_COMB.seq: *
2: /cgn2_6/ptodata/2/lna/5b_COMB.seq: *
3: /cgn2_6/ptodata/2/lna/5b_COMB.seq: *
4: /cgn2_6/ptodata/2/lna/5b_COMB.seq: *
5: /cgn2_6/ptodata/2/lna/5b_COMB.seq: *
6: /cgn2_6/ptodata/2/lna/5b_COMB.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	124.8	9.6	486	3	US-08-493-071-13 Sequence 13, Appl
2	124.8	9.6	564	3	US-08-493-071-12 Sequence 12, Appl
3	124.8	9.6	711	3	US-08-493-071-11 Sequence 11, Appl
4	124.8	9.6	798	3	US-08-493-071-14 Sequence 14, Appl
5	124.8	9.6	840	2	US-08-690-457-14 Sequence 14, Appl
6	124.8	9.6	840	2	US-08-628-187-14 Sequence 14, Appl
7	124.8	9.6	867	2	US-08-690-457-13 Sequence 13, Appl
8	124.8	9.6	867	2	US-08-628-187-13 Sequence 13, Appl
9	124.8	9.6	870	2	US-08-690-457-12 Sequence 12, Appl
10	124.8	9.6	870	2	US-08-628-187-12 Sequence 12, Appl
11	124.8	9.6	2940	1	US-08-690-457-15 Sequence 15, Appl
12	124.8	9.6	2940	2	US-08-628-187-15 Sequence 15, Appl
13	121.6	9.4	911	1	US-08-393-985-5 Sequence 15, Appl
14	117.2	9.1	790	1	US-08-393-985-22 Sequence 22, Appl
15	117.2	9.1	2097	1	US-08-393-985-1 Sequence 1, Appl
16	107.2	8.3	1200	1	US-08-356-397-1 Sequence 1, Appl
17	107.2	8.3	3000	1	US-08-393-985-3 Sequence 3, Appl
18	94.4	7.3	486	3	US-08-493-071-9 Sequence 9, Appl
19	94.4	7.3	564	3	US-08-493-071-8 Sequence 8, Appl
20	94.4	7.3	711	3	US-08-493-071-7 Sequence 7, Appl
21	94.4	7.3	795	3	US-08-493-071-10 Sequence 10, Appl
22	94.4	7.3	834	1	US-08-690-457-8 Sequence 8, Appl
23	94.4	7.3	834	2	US-08-628-187-8 Sequence 8, Appl
24	94.4	7.3	864	1	US-08-690-457-7 Sequence 7, Appl
25	94.4	7.3	864	1	US-08-628-187-7 Sequence 7, Appl
26	94.4	7.3	867	1	US-08-690-457-6 Sequence 6, Appl
27	94.4	7.3	867	2	US-08-628-187-6 Sequence 6, Appl

28	89.6	6.9	1054	1	US-08-393-985-7 Sequence 7, Appl
29	79	6.1	973	1	US-08-393-985-9 Sequence 9, Appl
30	64.8	5.0	7218	1	US-08-232-463-14 Sequence 14, Appl
31	58.4	4.5	10660	2	US-08-267-803B-8 Sequence 8, Appl
32	58.4	4.5	10660	4	US-09-041-886-16 Sequence 16, Appl
33	58	4.5	19124	2	US-08-487-826B-13 Sequence 13, Appl
34	57.8	4.5	5852	1	US-07-867-106-2 Sequence 2, Appl
35	57.6	4.4	1129	4	US-09-227-357-40 Sequence 40, Appl
36	57.2	4.4	2230	4	US-08-378-313-24 Sequence 24, Appl
37	55.2	4.3	2836	3	US-08-747-221B-24 Sequence 24, Appl
38	55.2	4.3	2836	3	US-08-747-221B-26 Sequence 26, Appl
39	55.2	4.3	2836	4	US-09-005-051-24 Sequence 24, Appl
40	55.2	4.3	2836	4	US-09-005-051-26 Sequence 26, Appl
41	55	4.2	1558	1	US-08-455-550-7 Sequence 7, Appl
42	54.4	4.2	1736	3	US-09-182-816-72 Sequence 22, Appl
43	54.4	4.2	1736	3	US-09-182-816-72 Sequence 24, Appl
44	54.4	4.2	1736	3	US-09-471-528-22 Sequence 22, Appl
45	54.4	4.2	1736	3	US-09-471-528-24 Sequence 24, Appl

ALIGNMENTS

```
RESULT 1
US-08-493-071-13
: Sequence 13, Application US/08493071
: Patent No. 6127149
:
: GENERAL INFORMATION:
: APPLICANT: Hirai, Yohei
: APPLICANT: Koshida, Shogo
: APPLICANT: Oka, Yumiko
: TITLE OF INVENTION: MODIFIED EPI-MORPHIN
: NUMBER OF SEQUENCES: 30
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER
: STREET: 99 CANAL CENTER PLAZA, SUITE 300
: CITY: ALEXANDRIA
: STATE: VA
: COUNTRY: USA
: ZIP: 22314
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/493,071
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Price, Robert L.
: REGISTRATION NUMBER: 22,685
: REFERENCE/DOCKET NUMBER: 715-107
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-684-1111
: TELEFAX: 703-684-1124
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 486 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
:
: US-08-493-071-13
:
: Query Match 9.6%; Score 124.8; DB 3; Length 486;
: Best local similarity 60.7%; Pred. No. 5e-19;
: Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;
:
: QY 1 atccagcgcagctgagatcatgagcaagaagcttcgagcgcagcagatcgagagatcg 60
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: Db 133 atccagcgcagctgagatcatgagcaagaagcttcgagcgcagcagatcgagagatcg 192
```

Db 418 CTGGAGACGGGAGAGCCGTCATCTTATCTCGGATATTATATGATTTCACAAATCACT 477
QY 121 cgggcccctcaacgagatcgagagccgacccgagactgctgccttggaagccgc 180
Db 478 AGGCAAGCTCTCATGATGATCGATGCCGCCACAAGACATCATGAGCTGGAGACACAGC 537
QY 181 atccgcgacgtacagagctctcttcgtcagatgagtgagtgctggtgaggaagccgac 240
Db 538 ATCCGAGAGCTGCACGAGATGTTTCATGATATGCGCATGTTTGTTCGAGACTCAAGGTGAA 597
QY 241 accctgaagctatcgagctcaacgataaagaagcgtgactacaccgcccagggccaag 300
Db 598 ATGGTCAACAACATCGAGAGAAATGTGCTGACTCTGTATGATTATTCGTGAACATGCCAAG 657
QY 301 ggcgaggtgcggaagcgctgctgactgacgaaggaag 336
Db 658 GAAGAGACGAGAGAAAGCCATCAATATACGAGACGAG 693

RESULT 4
US-08-493-071-14
; Sequence 14, Application US/08493071
; Patent No. 6127149

GENERAL INFORMATION:
APPLICANT: Hitachi, Yohsei
APPLICANT: Koshida, Shogo
APPLICANT: Oka, Yumiko
TITLE OF INVENTION: MODIFIED EPIMORPHIN
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER
STREET: 99 CANAL CENTER PLAZA, SUITE 300
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/493,071
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Price, Robert L.
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 715-107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1124
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 798 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-493-071-14

Query Match 9.6%; Score 124.8; DB 3; Length 798;
Best Local Similarity 60.7%; Pred. No. 6,1e-19;
Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 1 atccagcgccagctgagatcaatggaagaagcttcggcgaccacagatcgagagacatg 60
Db 445 ATCCAGCGCCAGCTGAGATCACTCTGGAGGACCACTGACGAGAGAGCTGGAAGAGATG 504
QY 61 ttccagcaggtaagtggaagctgtttcccgagaaactgtgctgcgacgtgaaggcgcg 120

Db 505 CTGAGAGACGGGAGAGCCGTCATCTTATCTCGGATATTATATGATTTCACAAATCACT 564
QY 121 cgggcccctcaacgagatcgagagccgacccgagactgctgccttggaagccgc 180
Db 565 AGGCAAGCTCTCATGATGATCGATGCCGCCACAAGACATCATGAGCTGGAGACACAGC 624
QY 181 atccgcgacgtacagagctctcttcgtcagatgagtgagtgctggtgaggaagccgac 240
Db 625 ATCCGAGAGCTGCACGAGATGTTTCATGATATGCGCATGTTTGTTCGAGACTCAAGGTGAA 684
QY 241 accctgaagctatcgagctcaacgataaagaagcgtgactacaccgcccagggccaag 300
Db 685 ATGGTCAACAACATCGAGAGAAATGTGCTGACTCTGTATGATTATTCGTGAACATGCCAAG 744
QY 301 ggcgaggtgcggaagcgctgctgactgacgaaggaag 336
Db 745 GAAGAGACGAGAGAAAGCCATCAATATACGAGACGAG 780

RESULT 5
US-08-690-457-14
; Sequence 14, Application US/08690457
; Patent No. 5726298

GENERAL INFORMATION:
APPLICANT: BIOMATERIAL RESEARCH INSTITUTE CO., LTD.
TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE SUBSTANCE
DESIGNATED AS EPIMORPHIN, GENES ENCODING THE SAME, AND AN
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: 1, Taya-cho, Sakae-ku, Yokohama-shi, KANAGAWA,
STREET: 1, Taya-cho
CITY: Yokohama-shi
COUNTRY: Japan
ZIP: 244
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,457
FILING DATE: 16-AUG-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/078,309
FILING DATE: June 15, 1993
APPLICATION NUMBER: 294856/1991
FILING DATE: October 16, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 294857/1991
FILING DATE: October 16, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 122906/1992
FILING DATE: April 17, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 135692/1992
FILING DATE: April 30, 1992
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 840
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-690-457-14

Query Match 9.6%; Score 124.8; DB 1; Length 840;
Best Local Similarity 60.7%; Pred. No. 6,2e-19;
Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

MOLECULE TYPE: CDNA
US-08-690-457-13

Query Match
Best Local Similarity 60.7%; Pred. No. 6.3e-19;
Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

9.6%; Score 124.8; DB 1; Length 867;
1 atccagcgccagctgagatcatgcaagaagtcctcgcgccagccagcagatg 60
|||||
445 ATCCAGCGCCAGCTGGAGATCACTGGGAGAGACACCACTGACGAGCTGGAAGATG 504
61 ttcagcagagtgtaagtcggagcgtgtttccgagaactgctgycgcagcgtgaaggcg 120
|||||
505 CTGGAGAGCGGAGCGGAGCGCTCATCTTCGGAATATATATACGATTCACAATAC 564
121 cggcgccctcaagcagatcgagagccgcagcagcagcagcagcagcagc 180
|||||
565 AGGCAAGCTCTCAATGATCGAGTCCCGCCACAAGACATCATGAGCTGGAGAC 624
181 atccgagcgtacacgagctctcttcgagatgcyggtgctggtgagaaagcagccgac 240
|||||
625 ATCCGAGACTGCACGAGATGTCATGATGATGCGCATGTTTGCAGACTCAGGTGAA 684
241 accctgaagctcagcagcctctcttcgagatgcyggtgctggtgagaaagcagccgac 300
|||||
685 ATGTCACCAACATCGAGAGAAATGTGTAACCTGTGTAATTAACGTGAACATGCCAAG 744
301 ggcgaggtcggaagccgctgagtaagcagagagaag 336
|||||
745 GAAGAGACGAGAAAGCCATCAATACCAAGCAAG 780

RESULT 8

US-08-628-187-13
Sequence 13, Application US/08628187

Patent No. 5837239

GENERAL INFORMATION:

APPLICANT: BIOMATERIAL RESEARCH INSTITUTE CO., LTD.
TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE SUBSTANCE DESIGNATED
TITLE OF INVENTION: AS EPIMORPHIN, GENES ENCODING THE SAME, AND ANTIBODIES THEREOF

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESSES:

ADDRESSEE: 1, Taya-cho, Sakae-ku, Yokohama-shi, KANAGAWA, Japan

STREET: 1, Taya-cho

CITY: Yokohama-shi

COUNTRY: Japan

ZIP: 244

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/628,187

FILING DATE: April 5, 1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 294856/1991

FILING DATE: October 16, 1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 294857/1991

FILING DATE: October 16, 1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 122906/1992

FILING DATE: April 17, 1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 135692/1992

FILING DATE: April 30, 1992

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 867

TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-628-187-13

Query Match
Best Local Similarity 60.7%; Pred. No. 6.3e-19;
Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

9.6%; Score 124.8; DB 2; Length 867;
1 atccagcgccagctgagatcatgcaagaagtcctcgcgccagccagcagatg 60
|||||
445 ATCCAGCGCCAGCTGGAGATCACTGGGAGAGACACCACTGACGAGCTGGAAGATG 504
61 ttcagcagagtgtaagtcggagcgtgtttccgagaactgctgycgcagcgtgaaggcg 120
|||||
505 CTGGAGAGCGGAGCGGAGCGCTCATCTTCGGAATATATATACGATTCACAATAC 564
121 cggcgccctcaagcagatcgagagccgcagcagcagcagcagcagcagc 180
|||||
565 AGGCAAGCTCTCAATGATCGAGTCCCGCCACAAGACATCATGAGCTGGAGAC 624
181 atccgagcgtacacgagctctcttcgagatgcyggtgctggtgagaaagcagccgac 240
|||||
625 ATCCGAGACTGCACGAGATGTCATGATGATGCGCATGTTTGCAGACTCAGGTGAA 684
241 accctgaagctcagcagcctctcttcgagatgcyggtgctggtgagaaagcagccgac 300
|||||
685 ATGTCACCAACATCGAGAGAAATGTGTAACCTGTGTAATTAACGTGAACATGCCAAG 744
301 ggcgaggtcggaagccgctgagtaagcagagagaag 336
|||||
745 GAAGAGACGAGAAAGCCATCAATACCAAGCAAG 780

RESULT 9

US-08-690-457-12
Sequence 12, Application US/08690457

Patent No. 5726298

GENERAL INFORMATION:

APPLICANT: BIOMATERIAL RESEARCH INSTITUTE CO., LTD.
TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE SUBSTANCE
TITLE OF INVENTION: DESIGNATED AS EPIMORPHIN, GENES ENCODING THE SAME, AND AN

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESSES:

ADDRESSEE: 1, Taya-cho, Sakae-ku, Yokohama-shi, KANAGAWA,

STREET: 1, Taya-cho

CITY: Yokohama-shi

COUNTRY: Japan

ZIP: 244

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/690,457

FILING DATE: 16-AUG-1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/078,309

FILING DATE: June 15, 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 294856/1991

FILING DATE: October 16, 1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 294857/1991

FILING DATE: October 16, 1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 122906/1992

FILING DATE: April 17, 1991

PRIOR APPLICATION DATA:

;; FILING DATE: October 16, 1991
;; PRIOR APPLICATION DATA: 294857/1991
;; FILING DATE: October 16, 1991
;; PRIOR APPLICATION DATA: 294857/1991
;; APPLICATION NUMBER: 122906/1992
;; FILING DATE: April 17, 1991
;; PRIOR APPLICATION DATA: 135692/1992
;; FILING DATE: April 30, 1992
;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2940
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
US-08-690-457-15

Query Match 9.6%; Score 124.8; DB 1; Length 2940;
Best Local Similarity 60.7%; Pred. No. 1.1e-18;
Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 1 attcaagcgccagctgtagatcatgagcaagaagttctcgagcgaccagatcgagagcatg 60
|||||
DB 597 ATCCAGCGCCAGCTGGAGTGCACCTGCGAGCACCACTGACGAGCTGGAGAGATG 656
QY 61 ttcgagcaggtagtggagcgtgtttccgagaactgctgagcgagctgaaaggcg 120
|||||
DB 657 CTGGAGAGCGGGAAGCCGTCATCTTCATCTCGATATTATATCAGATTCAAAATCACT 716
QY 121 cggcgccctcaacagatcgagagcgccagcggaactgctgagccttgagaagcg 180
|||||
DB 717 AGCAAGCTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 776
QY 181 atccgagcagctacagagcctctcttcgagatgagcggtgctggtgagaagcagcg 240
|||||
DB 777 ATCCGAGAGCTGACGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 836
QY 241 accctgaagctacagagcagctacagagcagctgagctacagcgagcgagcg 300
|||||
DB 837 ATGCTCAACAACATCGAGAAATGTGTGATCTGTAGATTACGTGGAATGCCAAG 896
QY 301 gcgcaggtgcggaagcgctgagctgagctgagctgagctgagctgagctgagctg 336
|||||
DB 897 GAAGAGAGCAAGAAAGCCATCAATACCAAGCAAG 932

ULF 12

08-628-187-15
Sequence 15, Application US/08628187
Patent No. 5837239

GENERAL INFORMATION:

APPLICANT: BIOMATERIAL RESEARCH INSTITUTE CO., LTD.

TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE SUBSTANCE DESIGNATED

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESS: 1, Taya-cho, Sakae-ku, Yokohama-shi, KANAGAWA, Japan

STREET: 1, Taya-cho

CITY: Yokohama-shi

COUNTRY: Japan

ZIP: 244

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

;; PRIOR APPLICATION DATA: 294856/1991
;; FILING DATE: October 16, 1991
;; PRIOR APPLICATION DATA: 294857/1991
;; APPLICATION NUMBER: 122906/1992
;; FILING DATE: April 17, 1991
;; PRIOR APPLICATION DATA: 135692/1992
;; FILING DATE: April 30, 1992
;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2940
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
US-08-628-187-15

Query Match 9.6%; Score 124.8; DB 2; Length 2940;
Best Local Similarity 60.7%; Pred. No. 1.1e-18;
Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 1 attcaagcgccagctgtagatcatgagcaagaagttctcgagcgaccagatcgagagcatg 60
|||||
DB 597 ATCCAGCGCCAGCTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 656
QY 61 ttcgagcaggtagtggagcgtgtttccgagaactgctgagcgagctgaaaggcg 120
|||||
DB 657 CTGGAGAGCGGGAAGCCGTCATCTTCATCTCGATATTATATCAGATTCAAAATCACT 716
QY 121 cggcgccctcaacagatcgagagcgccagcggaactgctgagccttgagaagcg 180
|||||
DB 717 AGCAAGCTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 776
QY 181 atccgagcagctacagagcctctcttcgagatgagcggtgctggtgagaagcagcg 240
|||||
DB 777 ATCCGAGAGCTGACGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 836
QY 241 accctgaagctacagagcagctacagagcagctgagctacagcgagcgagcg 300
|||||
DB 837 ATGCTCAACAACATCGAGAAATGTGTGATCTGTAGATTACGTGGAATGCCAAG 896
QY 301 gcgcaggtgcggaagcgctgagctgagctgagctgagctgagctgagctgagctg 336
|||||
DB 897 GAAGAGAGCAAGAAAGCCATCAATACCAAGCAAG 932

RESULT 13

US-08-393-985-5
Sequence 5, Application US/08393985
Patent No. 5693476

GENERAL INFORMATION:

APPLICANT: Scheller, Richard H.

TITLE OF INVENTION: Methods and Compositions for Modulation

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESS: Dehlinger & Associates

STREET: 350 Cambridge Avenue, Suite 250

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 499)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps@remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/MLML at: www-bio.illn.gov/bhrp/image/image.html
The following repetitive elements were found in this cDNA sequence:
285-313, >AT-rich#low_complexity
Seq primer: M13 Forward.
Location/Qualifiers
1. 499
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3077288"
/clone_1lb="NIH_MGC_50"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: pRT3-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (3.5-4.4kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 140 a 96 c 62 g 201 t
ORIGIN

Query Match 32.2%; Score 416.4; DB 9; Length 499;
Best Local Similarity 99.5%; Pred. No. 4.3e-36;
Matches 428; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

835 gagcgaaatggccttgggaaacacgcttccttcgcgattccttcacggtctac 894
|||||
7 GAGCGAAATGGCCTTGGGAAACACGCTTCCTTCGATCTTCATCGGCTCAC 66
|||||
895 ggcctatgcaatcccccacaaatagatctattctgcctcattccctactattaa 954
|||||
67 -GCTATGCAATTCCTCCCAATATAGATCTTATTCGCTCATTTCCCTACTATTAA 125
|||||
955 aatcaccaacaaccttctattctctctccttcacctttaaatacttcacag 1014
|||||
126 AATCACCAACAACCTTCTATTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCA 185
|||||
1015 gtaataattgtaataatttccaacaattttaagcaactgaataatcgaagaacgac 1074
|||||
186 GTTATATTTTGGTATTTATTTTCCAAACATTTTAAAGCAGCTGAATATGCAACAGACATC 245
|||||
1075 aaatgaagatcagatcgtttgtgtatatttccgcgtgataaataattactaa 1134
|||||
246 AAAATTGAAGTATCACTGTTTGTGATTTTGTGATTTTGTGATTTTGTGATTTTAA 305
|||||
1135 tattttactgattacatgacatgataatgtaagtgaataactaataattcacta 1194
|||||
306 TATTTTACTTGATTTACATATGACATGATGATGATGATGATGATGATGATGATGAT 365
|||||
1195 atatgtacataatgataatggttttaactcttattatgtaagtaatgataatc 1254
|||||
366 ATATGTACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 425
|||||

QY 1255 aagacgaana 1264
Db 426 AAGACGAACA 435

RESULT 13
LOCUS BF893543
DEFINITION QV1-MT0132-131100-473-g06 MT0132 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF893543
VERSION BF893543.1 GI:12285106
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 429)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Baia, G. S., Simpson, D. H., Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV1&t2=QV1-MT0132-131100-473-g06&t3=2000-11-13&t4=1>)
Seq primer: puc 18 forward
High quality sequence stop: 429.
Location/Qualifiers
1. 429
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1lb="MT0132"
/dev_stage="Adult"
/note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 91 a 144 c 135 g 59 t
ORIGIN

Query Match 31.1%; Score 403; DB 10; Length 429;
Best Local Similarity 99.8%; Pred. No. 1.3e-34;
Matches 414; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

99 gctggcgaagctgaaagggcgcgccctcaagagatcgaagccgcacgcga 158
|||||
16 GCTGGCGACGTGAAGGGCGCGCGCCGCCCTCAACAGAGATGAGAGCCGCCACCGCA 75
|||||
159 actgctgcgcctggagagcgatcgcgagcaacgagctctcttcagatggcgt 218
|||||
76 ACTGCTGCCCTGGAGAGCGCATCCGACACGACAGACTCTTCTTCTTCTTCTTCTTCTTCT 135
|||||
219 gctgtgtggaagcgaagccgacacccctgaacgctcagcgtcaacgtaacaaagcgt 278
|||||
136 GCTGTGTGGAAGCAGAGCCGACACCTTGAAACGTCATCGAGCTCAACGTACAAAGACGCT 195
|||||

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 24, 2002, 12:53:01 : Search time 1809.41 Seconds

(without alignments)
9659.810 Million cell updates/sec

Title: US-09-762-249-13

Perfect score: 1295

Sequence: 1 atccagcgcgcgtcgtgagat.....aaaaaaaaaaaaaaaaaa 1295

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :
EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inu:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	728	56.2	739	10	B1518895 603061815
2	658.6	50.9	911	10	B1519530 603061815
3	543.2	41.9	571	10	BM149627 TCAP3D91
4	521	40.2	598	10	BF892936 OVI-MT013
5	487.4	37.6	525	10	BF894780 OVI-MT013
6	465.4	35.9	525	10	BF892927 OVI-MT013
7	456.4	35.2	480	10	BF195864 7086C04.x
8	447.8	34.6	470	9	A1275149 q170h12.x
9	443.8	34.0	464	10	BF893539 OVI-MT013
10	429.6	33.2	434	9	AA026277 wv1a05.x
11	421.4	32.5	434	9	AA227632 zt98h02.r
12	416.4	32.2	499	9	AA500047 UT-HF-BNO
13	403	31.1	429	10	BF893543 OVI-MT013
14	402.4	31.1	426	9	AA262151 z523d09.r
15	397.2	30.7	2219	11	AK017897 Mus muscu
16	393.4	30.4	406	9	AA662909 h183c07.x
17	384	29.7	409	9	AA500048 UI-HF-BNO

C	18	338	26.1	384	9	AA262016
C	19	308.4	23.8	310	9	AA500436
C	20	308	22.9	352	12	AQ988258
C	21	296.6	22.3	361	10	R64498
C	22	294.2	22.7	417	9	AM784298
C	23	269.8	20.8	821	10	BG247715
C	24	235.6	18.2	452	10	R33852
C	25	228.4	17.6	547	12	A2966926
C	26	205.8	15.9	339	10	R33851
C	27	202	15.6	484	9	AA499912
C	28	194.4	15.0	820	10	BF165171
C	29	190.2	14.7	356	10	R65594
C	30	149	11.5	149	9	AA213862
C	31	148.4	11.5	583	10	B1776010
C	32	133.8	10.3	149	10	T25062
C	33	118.4	9.1	656	10	BE798232
C	34	114.4	8.8	812	10	BF784996
C	35	113	8.7	889	11	AK009770
C	36	111.4	8.6	527	9	BE200283
C	37	111	8.6	509	9	BB363966
C	38	109.6	8.5	535	10	BG911547
C	39	108	8.3	451	10	BF041469
C	40	108	8.3	954	10	BE799709
C	41	107.6	8.3	691	10	B1546649
C	42	103	8.0	466	9	AA504759
C	43	101.6	7.8	176	10	BF893531
C	44	101.2	7.8	469	10	BG730112
C	45	100.8	7.8	674	10	BG070771

ALIGNMENTS

RESULT 1
LOCUS B1518895
DEFINITION 603061815F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5211074 5', mRNA sequence.
VERSION B1518895
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/
AUTHORS 1 (bases 1 to 739)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1AM1529 row: n column: 03
High quality sequence stop: 738.
Location/Qualifiers
1..739
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5211074"
/clone_lib="NIH_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH10B"
/note="Vector: pCMV-Sport6, Site:1: NotI; Site:2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range

Query Match	37.6%	Score 487.4	DB 10	Length 525
Best Local Similarity	99.6%	Pred. No. 1e-43		
Matches 499	Conservative 0	Mismatches 1	Indels 1	Gaps 1
OY	155	gcgaactgtctgcgcctgcggagagccgcatccgcgaactacagagctctcttcgcaatg	214	
Db	525	GGGAAGCTGTGGGCGCTGGAGAGCGCGCATCCGCACTTACACGAGCTCTTCTTGCACATGG	466	
OY	215	cggtctgtgtgtagaagaagcagcgcgcacccctgaacgtcatcgaactcaacgltacaaaga	274	
Db	465	CGGTGTGTGTGGTAGAGCAGCAGCGCCGACACCCCTGAACGTCAATCAGAGCTTCAACGTAAGA	406	
OY	275	cggtgcacacacacccggccagcagcagcgaagtgcgagagcgcgcgtgcagtagagaga	334	
Db	405	CGGTGCACATACACCGGCGCAGGCCAGAGCCGAGGTGGGAGAGCCGCTGACGTACGAGAGA	346	
OY	335	agaacccctgcgcgaacccctctgctctctctctctctctctctctctctctctctctctct	394	
Db	345	AGAACCCCTGCGCGGAGACCCCT	286	
OY	395	cggtgcgcacacccgcgcacccatcccaacgaatgagcgcgtgcgtagaagagcgtcaccaacgc	454	
Db	285	CGGGCGCGCACCGCCCATCCAGACCATGAGCGGCGCTGGAGAGACG-CACCAAGCGCG	227	
OY	455	ggagctctgcctctcaaggagatgtcccaaccccttccggaactcaatgtctttagaaga	514	
Db	226	GGAGCTCTGCGCTGCGAGGAGTGTCCCAACCCCTTCCGGAACCTCAAGTTTAGAAGAA	167	
OY	515	aacgcacaggttcaagaatctgaacacacgcgtgtctctgtagaagatggttagttacgc	574	
Db	166	AACGCAGGTTCAGAAATGCAACACGCGCTGTCTGTGAAAGATGTAGTTGATACCG	107	
OY	575	tcgcattgattcttcagtaagatagattcccaacaagtgtgcaatgtcatatataatgaca	634	
Db	106	TCCGATGATTTCTTCAAGTAAGATAGATTCCCAAGTTGTCAATGTCAATATATATGACA	47	
OY	635	ccctgcacatctaccgctctg 655		
Db	46	CTTGCACCTTACCGCTTAG 26		
RESULT	6			
LOCUS	BF892927/c			
DEFINITION	QV1-MT0132-081100-443-a05 MT0132 Homo sapiens CDNA, mRNA sequence.	525 bp	mRNA	linear EST 18-JAN-2001
VERSION	BF892927			
KEYWORDS	BF892927.1 GI:12284386			
SOURCE	EST.			
ORGANISM	human.			
REFERENCE	Enkayota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 525)			
AUTHORS	Dias Neto, E., Garcia Correa, R., Verlovski-Almeida, S., Britones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldmann, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.			
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)			
MEDLINE	20202663			
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL			

FEATURES	source	Location/Qualifiers
FEATURES	source	1..525
	/organism="Homo sapiens"	
	/db_xref="taxon:9606"	
	/clone_lib="MT0132"	
	/dev_stage="Adult"	
	/note="Organ: marrow; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 1997, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."	
BASE COUNT	95 a 146 c 158 g 126 t	
ORIGIN		
Query Match	35.9%	Score 465.4; DB 10; Length 525;
Best Local Similarity	99.0%	Pred. No. 2.3e-41;
Matches 500; Conservative	0; Mismatches 1;	Indels 4; Gaps 3;
QY	152 accgcgaactgctgtgcctcgtgagagccgcacatccgcgaactacagactctcttcgcaga	211
Db	525 ACCGGGAACTGCTGGCGCTGGAGACCCCATCCGGACGTACACCAAGCTCTTCTTGCCAGA	466
QY	212 tggcggtgctgtgttgagagaagcagcgccgcacacccctgaaagtcagctcgaagtcacaa	271
Db	465 TGGCGGTGCTGTGTGGAGAGAGCGCCGACACCCCTGAACGTCACTGAGCTCAACGTACAA	406
QY	272 agagagctgcactaacccgcgcgaagcgcaagggcgagtgctggaagggcgctgcaatcagag	331
Db	405 AGACGCTGACTATACCCGCGCAGGCCAAGGGCGCAGGTGCGGAAGCCGCTGCAGTACGAGG	346
QY	332 agaagaacccctcgcgcgaacctctgtctcttctgtctgtccctgcctcgaagtagcagggcg	391
Db	345 AGAATAACCCCTCGCGGACCCCTCTCTGCTTCTGCTGTCTGCTCTCAAGTACGAGGCCG	286
QY	392 gccgcggcgccgcacccgcacatccacagacatgagcgcgctgtggaagagcgttcaccaaag	451
Db	285 GCCCGGGCGCCGACCGCCCATCCAGACCATGAGAGCGCGGTGGGAAGAGCG-CACCAAG	227
QY	452 ccggagagctctgcctctgagggagtgctccccaaccccttcgcgaactcgaagtccttagaa	511
Db	226 CCGGAGAGCTTGTCCCTCGAGGGAGTGTGCCCAACCTTTCGGAACTCAGTCTTTAGCAA	167
QY	512 agaagcgccaggttcaagaatctgcaaacaccgcctgtgc-ttggaagaagtggttagtat	570
Db	166 AGAAACGCCAGGTTTCAGAAATTGCCAACCAACAGCTGTGGTGGAAAGTGGTATTGATT	107
QY	571 accgtccgaatgattcttcagtaagaatagattcccaacaagtctgtgcaatgtcattat	630
Db	106 ACCGTCGATGATCTTCTCAGTAAAGATGATTTCCACAAATTTGGCAA--TCATTATAT	49
QY	631 gaaacactgcacacttcaacgctcttg 655	
Db	48 GACACCTTGCACTCTTACCGCTCTAG 24	
RESULT 7	BF195864/c	480 bp mRNA linear EST 03-NOV-2000
LOCUS	BF195864	7086c04.x1 NCI-CPAP_Kid11 Homo sapiens cDNA clone IMAGE:3643015 3'
DEFINITION	mRNA sequence.	
ACCESSION	BF195864	
VERSION	BF195864.1	GI:11083169
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	

[illegible]

REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	COMMENT
1 (bases 1 to 464)	Dias Neto, E., Garcia Correia, R., Veljovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bal, G.S., Simpson, D. H., Brunslein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags	Proc. Natl. Acad. Sci. U.S.A.	97 (7), 3491-3496 (2000)	
2020263	Contact: Simpson A.J.G.				

Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel.: +55-11-2704922
Fax: +55-11-2707001
Email: asimposon@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?pl=GV16t2-GV1-MF0132>
131100-473-e106t3-2000-11-136t4-1)
Seq primer: puc 18 forward
High quality sequence stop: 464.

```

FEATURES
  source
    Location/Qualifiers
      1..464
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone_idb="MT0132"
        /dev_stage="Adult"
        /note="Organ: marrow; Vector: puc18; Site.1: Sma1; Site.2:
Sma1; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent Application No. 196
, 716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT
  103 a 153 c 143 g 65 t
ORIGIN

```

Query Match 34.0%; Score 439.8; DB 10; Length 464

Best Local Similarity -98.3%; Pred. NO. 1.4e-38;
Matches 455; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY	87	ttccggaactctgtcgcgcgaagtcbaaagggcgcgggccgcctcaacgaatcgaag	146
Db	3	TTACGCTGAGCGGCTGGCCGACGTGAAGGGCGCGGCCGCCCTCAAGAGATGAGAG	62
QY	147	ccgcaccgcggaactgtctgtgccttggagagccgcataccgagctacagactcttc	206
Db	63	CCGGCCACCGCCCAACTGCTGCGCCCTGGAGAGCGCGCTTCGGCGACGTACAGACTTCTT	122
QY	207	gcagatgcggtgtctgtgtgtagaagcagcgccagaccccttgacgtcatcgaatcaagt	266
Db	123	GCAATGGCGGTGCTGTGTGTGGAGAAAGCAGGCCGACACCTTGAACTGATCGAGCTTAACT	182
QY	267	acaaagacagcttcgactacacccggccaggccaaagcgcaagctgcgaaagcgcttga	326
Db	183	ACAAAAGACGGTTCGACTACACCGGCCAAGCCCAAGCGCAGGTGCGAAGGCCGTGACATA	242
QY	327	cgagagagaagaacccctcgcggaacctctgtctgtctgtccctcctcaagtaaga	386
Db	243	CGAAGAGAAAGAACCCCTGCTCCCGACCCCTTGCTGTGCTGTCCCTTCCTCAATATACA	302
QY	387	ggccggccccggcgccgaacgcgccatcccacagacaatgaagcgcgcttggaaagacgtac	446
Db	303	GGCCGGCCCCGGGCCGCCACGCCCATCCCAACCATGAGAGCGCGCTGGGAAGAGACG-CAC	361
QY	447	caaaagccggagactctgcctctcagaggaattgcccacaaccttlccggaactcagctct	506
Db	362	CAAGCGGGAGGACTCTGGCCCTCGCAGGGAGTGGCCCAACCCCTTTCGGGAATCATGCTTT	421
QY	507	agaaagaaagcgcgaagttcaagaatttgcacaacgaagctctgtgc	549
Db	422	AGAAAGAAAGCCCAAGGTTCAAGATTGCCAACACCGCTGTGC	464

RESULT	10
LOCUS	AM026277/c
DEFINITION	462 bp mRNA linear EST 27-OCT-1998 w118405.x1 NCI-CGAP_Brn23 Homo sapiens cDNA IMAGE:2529200 3'
ACCESSION	AM026277
VERSION	AM026277
KEYWORDS	mRNA sequence.
SOURCE	AM026277.1 GI:5879807
ORGANISM	EST. human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Ethulia; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 462)
REFERENCE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS	National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
TITLE	Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D.

FEATURES

source

Email: cgapns-remail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/brpr/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 442.
Location/Qualifiers
1. 462
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2529200"
/clone_1lb="NCI_CGAP_Brn23"
/tissue_type="gliblastoma (pooled)"

CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393.985
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600-0152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2097 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Rat syntaxin 1A 3' end (encoding amino
INDIVIDUAL ISOLATE: acids 4-288; GenBank M95734)
FEATURE:
NAME/KEY: CDS
LOCATION: 2..859
US-08-393-985-1

Query Match 9.1%; Score 117.2; DB 1; Length 2097;
Best Local Similarity 58.2%; Pred. NO. 4.5e-17;
Matches 206; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

Qy	1	atccagcgccagctgagatcgtggcaaggagtcctcgggcgaccagatcgaggacatg	60
Db	437	ATCCAGAGCGCAGCTGGAGATCACTGGCCGCGCACCCAGCAGTGGAGAGTGGAGACATG	496
Qy	61	ttcggagcagggtaagtggagcgtgtttccgagaaacttggccgcacgtgaaggcgcg	120
Db	497	CTGGAGAGTGGGAATCCGCCATCTTGGCTCTGGGATCATGACATCCAGCATCTCG	556
Qy	121	cgggcgccctcaacgagatcgagagccgcaccgcgaactgctgcctggagagccgc	180
Db	557	AAGCAGGCGCTCAGTCAGATCGAGACGAGCAGGACAGTGAATCAAGTTGGAGACAGC	616
Qy	181	atccgagcgtacacagctcttcttgagatggcggtgctggtggaagcagccgac	240
Db	617	ATCCGGGAGCTACAGATATGTTCATGGACATGGCCATGTCGTGGAGAGCCAGGGGGAG	676
Qy	241	accctgaacctcatcgagctcaacgtacaaagacggtcgactacaccgagcccaag	300
Db	677	ATGATTGACAGGATCGAGTACAAATGTGGAACACCGCTGTGGACTACGTGGAGGGCCGTG	736
Qy	301	gcgcagggtgcgaagccgtgcagctacagaggagagaacccctgccggaccctc	354
Db	737	TCTGACACCAAGAGGCGCTCAAGTACCAGACGCAAGCGCAGGAGGAAGATC	790

Search completed: September 24, 2002, 15:00:52
Job time: 2930 sec

